

**In the Claims:**

This listing of claims will replace all prior versions and listings of claims in the application:

1. (Currently Amended) A crystal comprising of a polypeptide having the amino acid sequence of residues 29-766 of SEQ ID NO: 2~~dipeptidyl peptidase IV~~ wherein the crystal diffracts x-rays for the determination of the atomic coordinates of the polypeptide at a resolution of 3 Å or less. ~~having characteristics sufficient to ensure a resolution capable of analyzing its three-dimensional structure up to the side chain level by X-ray crystallographic structural analysis.~~
2. (Cancelled)
3. (Currently Amended) The A crystal comprising a polypeptide having the amino acid sequence of residues 33-766 of SEQ ID NO: 2 wherein the crystal diffracts x-rays for the determination of the atomic coordinates of the polypeptide at a resolution of 3 Å or less. ~~according to claim 1 or 2, wherein the dipeptidyl peptidase IV is a polypeptide having an amino acid sequence in which a transmembrane region is deleted from the amino acid sequence of SEQ ID NO: 2, and a tag peptide is optionally added to a C-terminal side or N-terminal side thereof.~~
4. (Currently Amended) The crystal according to claim 1 or 3 ~~any one of claims 1 to 3~~, wherein the crystal has a space group of  $P2_12_12_1$ , and a lattice constant of the unit cell of  $|a| = 118.0 \pm 5.0 \text{ Å}$ ,  $|b| = 125.9 \pm 5.0 \text{ Å}$ ,  $|c| = 136.8 \pm 5.0 \text{ Å}$ , and  $\alpha = \beta = \gamma = 90^\circ$ , and is orthorhombic.
5. (Currently Amended) The crystal according to claim 1 or 3 ~~any one of claims 1 to 4~~, wherein the crystal has the structural coordinates shown in Figure 4.

6. (Currently Amended) The crystal according to claim 1 or 3 ~~any one of claims 1 to 4~~, wherein the crystal has a structural coordinates different from the structural coordinates as shown in Figure 4 via fluctuation of a protein.

7-24. (Cancelled)

25. (New) The crystal according to claim 1 or 3, wherein the polypeptide further comprises a polyhistidine tag.

26. (New) The crystal according to claim 1 or 3 wherein the crystal diffracts x-rays for the determination of the atomic coordinates of the polypeptide at a resolution of 2.8 Å or less.

27. (New) The crystal according to claim 1 or 3 wherein the crystal diffracts x-rays for the determination of the atomic coordinates of the polypeptide at a resolution of 2.6 Å or less.

28. (New) The crystal according to claim 1 or 3, wherein amino acid residues Ser 630, Asp 708 and His 740 of SEQ ID NO:2 have the structural coordinates shown in Figure 4.